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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,840BDATE: 03/11/2002
TIME: 09:51:56Input Set : A:\100564-09049.txt
Output Set: N:\CRF3\03112002\I424840B.raw

3 <110> APPLICANT: Berchtold, Peter
 4 Escher, Robert F. A.
 6 <120> TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
 8 <130> FILE REFERENCE: 100564-09049
 10 <140> CURRENT APPLICATION NUMBER: 09/424,840B
 11 <141> CURRENT FILING DATE: 1999-12-03
 13 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
 14 <151> PRIOR FILING DATE: 1998-05-08
 16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
 17 <151> PRIOR FILING DATE: 1997-12-12
 19 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
 20 <151> PRIOR FILING DATE: 1997-06-06
 22 <160> NUMBER OF SEQ ID NOS: 128
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 357
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(357)
 34 <223> OTHER INFORMATION:
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 40 1 5 10 15
 42 acc ctg tcc ctc aac tgc act gtc tct ggt cgc tcc atc agt ggt tac 96
 43 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 44 20 25 30
 46 tct tgg aga tgg atc cgg cag tct cca ggg aag gga cta gag tgg att 144
 47 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 48 35 40 45
 50 ggg gat atc tct tat agt ggg agt acc aag tac aaa ccc tcc ctc agg 192
 51 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 52 50 55 60
 54 agt cga gtc acc ctg tca gta gac acg tcc aag aac cag ttc tcc ctg 240
 55 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 56 65 70 75 80
 58 aag ctg aat tcg gtg acc gct gcg gac acg gcc gtc tat tac tgt gcg 288
 59 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 60 85 90 95
 62 cga gtc ttg ccc ttt gac ccg atc tcg atg gac gtc tgg ggc aaa ggg 336
 63 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly

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74	<213> ORGANISM: Homo sapiens			
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82	Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr			
83	20 25 30			
86	Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile			
87	35 40 45			
90	Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg			
91	50 55 60			
94	Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu			
95	65 70 75 80			
98	Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala			
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126	acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt			96
127	Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Arg Ser Asn Pro Val			
128	20 25 30			
130	agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt			144
131	Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe			
132	35 40 45			
134	ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc			192
135	Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
136	50 55 60			
138	aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg			240
139	Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly			
140	65 70 75 80			

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142 gat gct ggt gac tat tac tgt gca aca tgg gat gac ggc ctc aat ggt	288
143 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly	
144 85 90 95	
146 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc	333
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148 100 105 110	
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163 20 25 30	
166 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe	
167 35 40 45	
170 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
171 50 55 60	
174 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly	
175 65 70 75 80	
178 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly	
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182 Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro	
183 100 105 110	
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188 <212> TYPE: DNA	
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200 1 5 10 15	
202 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat	96
203 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
204 20 25 30	
206 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg	144
207 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
208 35 40 45	
210 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg	192
211 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
212 50 55 60	
214 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat	240
215 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
216 65 70 75 80	

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218	ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	acg	gct	gtg	tat	tac	tgt	288	
219	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
220																95		
221																	336	
222	gcg	aga	gca	gct	ctg	ggg	agc	tgg	ggg	ggt	tgg	gac	cac	tac	atg	gac	gtc	
223	Ala	Arg	Ala	Leu	Gly	Ser	Trp	Gly	Gly	Trp	Asp	His	Tyr	Met	Asp	Val		
224																110		
225																	369	
226	tgg	ggc	aaa	ggg	acc	acg	gtc	acc	gtc	tcc	tca							
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236																15		
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238																10		
239																		
240																		
241																		
242	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr		
243																		
244																30		
245																		
246	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
247																		
248																45		
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252																60		
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261	25																	
262	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
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283	1																	
284																		
285																15		
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295	Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
296	50	55	60	
298	aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag			240
299	Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu			
300	65	70	75	80
302	gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt			288
303	Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly			
304	85	90		95
306	tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc			333
307	Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro			
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312	<211> LENGTH: 111			
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322	Thr Ile Ser Cys Ser Gly Ser Ser Asn Ile Gly Ser Asn Thr Val			
323	20	25		30
326	Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr			
327	35	40		45
330	Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
331	50	55		60
334	Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu			
335	65	70		80
338	Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly			
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360	1	5	10	15
362	tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt			96
363	Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe			
364	20	25		30
366	gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc			144
367	Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
368	35	40		45
370	tca ggc att agt ggt ggt ctt ttg aca cac tac gca gac tcc gtg			192

VERIFICATION SUMMARY

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